Amendments to the Claims

This listing of claims replaces all prior versions of claims in the application.

1. (Withdrawn) A method for identifying a drug discovery target which comprises:

(a) providing a means for storing and accessing genomics information in a database wherein said means permits computational analysis of biological relationships among the stored concepts;

(b) querying the database to identify a disease-related pathway; and

(c) identifying the biological interactions and actor concepts in the disease related pathway whereby each of the actor concepts involved in each such reaction is a drug discovery target.

2. (Withdrawn) The method of claim 1 wherein the genomics information comprises information relating to genes, their DNA sequences, mRNA, the proteins that result when the genes are expressed, and the biological effects of the expressed proteins.

3. (Withdrawn) The method of claim 2 wherein the data comprise data extracted from multiple public sources.

4. (Withdrawn) The method of claim 2 wherein the data comprises proprietary data.

5. (Withdrawn) The method of claim 2 wherein the data comprises data extracted from a combination of proprietary and public data sources.

6. (Withdrawn) The method of claim 2 wherein the data comprises data extracted from a combination of proprietary and public data sources.

7. (Withdrawn) The method of claim 2 wherein the means for storing the genomics information includes an ontology in which:

(a) each gene, gene product, and biological effect is given an identifier which is related to synonyms for the identifier;

(b) each gene, gene product, and biological effect is categorized by class; and

(c) the relationship of each gene, gene product and disease state is defined by slots and facets.

8. (Withdrawn) The method of claim 2 wherein the candidate drug discovery targets in the disease related pathway are prioritized based on factors that include function and complexity.

9. (Withdrawn) The method of claim 8 wherein the candidate drug discovery targets are further prioritized based on markers for side effects and patient responsiveness.

10. (Withdrawn) The method of claim 2, further comprising combining the results of querying the database with the results of additional data obtained from one or more additional methods for identifying candidate drug discovery targets.

11. (Withdrawn) The method of claim 10 wherein the additional data is obtained from one of protein-protein interaction studies and protein profiling from mass spectrometry.

12. (Withdrawn) The method of claim 11 wherein the additional data is obtained from differential gene expression studies.

13. (Withdrawn) The method of claim 1 wherein the genomics information comprises information relating to genotype and the disease-related pathway comprises a gene or gene product associated with a particular genotype.

14. (Withdrawn) The method of claim 1 wherein the genomics information comprises the name of each gene, gene product, and their biological effects, and the means for storing and accessing the genomics information identifies relationships that are at least one step removed.

15. (Withdrawn) The method of claim 1, wherein the identifying the biological interactions step includes the step of comparing genomics data from the database to user-defined data using a statistical model.

16. (Withdrawn) The method of claim 15, wherein the comparing step includes identifying an overlap between user-defined data and data from the database and the statistical model is a statistical significance model measuring the likelihood that the overlap is a random event.

17. (Withdrawn) The method of claim 16, wherein the user-defined data is one of gene expression data and a manually entered gene list.

18. (Withdrawn) The method of claim 1, wherein the identifying the biological interactions step includes classifying one or more relevant findings using an ontology.

19. (Withdrawn) The method of claim 18, wherein the classifying one or more findings using an ontology includes determining a likelihood that the one or more findings residing in a particular biological classification in the ontology is statistically significant.

20. (Withdrawn) The method of claim 1, wherein the querying the database step includes the step of generating profiles according to one or more criteria.

21. (Withdrawn) The method of claim 20, wherein the profiles are pre-generated from the database.

22. (Withdrawn) The method of claim 20, wherein the profiles are generated by one of a data driven and model-driven approach.

23. (Withdrawn) The method of claim 20, wherein the profiles are gene-centric being derived about a central gene for all genes in the database.

24. (Withdrawn) The method of claim 20, wherein the profiles are at least one of process, function and disease centric being derived about a central biological process for all processes in the database.

25. (Withdrawn) The method of claim 20, wherein the profiles are at least one of tissue, organ or structure centric being derived about a central physical object for all object's in the database.

26. (Currently Amended) A computer system for evaluating user-supplied genomics data, the system comprising:

a computer comprising a structured database to store and access genomics information, wherein the structured database comprises stored genomics information, wherein the computer permits the computation of complex relationships among genes and/or gene products found within the genomics information;

wherein the computer is configured to:

(a) define [[a]] one or more profile models based on one or more profile definition criteria[[on]];

(b) pre-generate a profile library by building a collection of profiles according to the profile models using the genomics information stored in the structured database;

(c) receive the user-supplied genomics data;

(d)[[(c)]] identify one or more overlapped profiles from the profile library that overlap with at least a portion of the [[a]] user-supplied genomics data [[and]];

(e) determine, for each of the one or more [[such]] overlapped profiles, whether the overlap is statistically significant, wherein the determination permits all profiles to be compared in relative terms against each other; and

(f) [[(d)]] analyze one or more statistically significant overlapped profiles together with the user-supplied genomics data including inspection of database-asserted biological interactions embodied in the one or more statistically significant overlapped profiles;

wherein the computer system is a stand alone computer, a multicomponent computer, or a networked computer, and wherein the computer system further comprises hardware for electronically searching the structured database.

27. (Currently amended) The computer system of claim 26, wherein the computer is ~~further~~ configured to pre-generate a profile library containing a profile for each one of a genomic information type in the database according to the profile model.

28. (Previously Presented) The computer system of claim 27, wherein the profiles are pre-generated from a graph structure.

29. (Currently Amended) The computer system of claim 26, wherein the computer is further configured to generate the profiles by querying the structured database for information matching the one or more profile definition criteria~~on~~.

30. (Currently Amended) The computer system of claim 28, wherein the determination of whether the overlap is statistical significant~~ee includes~~ comprises the computation of a probability of overlap as a function of information contained in the structured database.

31. (Currently Amended) The computer system of claim 2726, wherein the genomic information is a type of information selected from the group consisting of ~~type is one of~~ a gene, gene product orand biological process.

32. (Currently Amended) The computer system of claim 26, wherein the user-supplied genomics data comprises~~is~~ differential gene expression data.

33. (Currently Amended) The computer system of claim 32, wherein the differential gene expression data relates to a ~~particular~~ disease.

34. (Currently Amended) The computer system of claim 26, wherein the one or more profile generation criteria~~on include~~ comprise one or more of a biological process, number of genes, organismal process, gene connectivity, edge connectivity, findings source type, experiment context, orand tissue consistency criterion.

35. (Previously Presented) The computer system of claim 26, wherein the profiles are generated from a seed node and the inspection of database-asserted biological interactions focuses on the biological interactions emanating from the seed node.

36. (Currently Amended) The computer system of claim 35, wherein the seed is selected from the group of genomic data types consisting~~one~~ of a gene, gene product, and biological process ~~genomic data type~~.

37. (Currently Amended) The computer system of claim 26, wherein the computer is further configured to compute a statistical significance for a biological association in the one or more ~~statistically significant~~overlapped profiles that are determined to comprise a statistically significant overlap.

38. (Currently Amended) The computer system of claim 27, wherein the pre-generation ~~pregeneration~~ of a profile library comprises~~includes, for each profile generated,~~ the selection of a node for a profile based on a~~the~~ number of similar findings in the structured database that link the node to a neighboring node.

39. (Currently Amended) The computer system of claim 26, wherein the computer is further configured to display information related to the one or more overlapped~~statistically significant~~ profiles that are determined to comprise a statistically significant overlap and the user-supplied genomics data using a GUI.

40. (Currently Amended) The computer system of claim 26, wherein the computer is further configured to annotate the profiles with biological associations asserted by the structured database wherein the associations comprise one or more of a cellular process, molecular process, organismal process orand disease process.

41. (Currently Amended) The computer system of claim 40, wherein the computer is further configured to display biological associations using one of a GUI orand a report.

42. (Currently Amended) The computer system of claim 40, wherein the annotation of profiles ~~includes~~ comprises ~~the~~ use of classification information found in an ontology.

43. (Currently Amended) The computer system of claim 26, wherein the determination of statistical significance ~~test~~ comprises~~includes~~ ~~athe~~ test of a null hypothesis over a discrete probability distribution, the distribution being a function of a size of the structured database~~size~~, sizes of profiles~~sizes~~, a size of the user-supplied genomics ~~data size~~ and expression values.

44. (Currently Amended) The computer system of claim 27, wherein the pre-generation ~~step~~ ~~includes~~ comprises generating a plurality of profile libraries and wherein each profile library corresponds to a different profile generation criterion.

45. (Withdrawn) A method for identifying a new use for a known therapy comprising the steps of providing a means for storing and accessing genomics information in a database wherein said means permits computational analysis of biological relationships among the stored concepts; querying the database to identify a disease-related pathway comprising a known therapy target; selecting at least one of such disease-related pathways wherein the known therapy target is also comprised within a second disease-related pathway; and identifying treatment of the second disease as a new use for the known therapy.

46. (Withdrawn) A method for prioritizing candidate development compounds for further development that comprises the steps of providing a means for storing and accessing genomics information in a database wherein said means permits computational analysis of biological relationships among the stored concepts; querying the database to identify all pathways associated with the target of each candidate development compound and assigning higher priority to development compounds on the basis of whether or not they are likely to result in an undesirable effect based on their involvement in other biological pathways.

47. (Withdrawn) A method for identifying disease-related pathways wherein the disease is a side effect of drug therapy that comprises the steps of providing a means for storing and accessing genomics information in a database wherein said means permits computational analysis of biological relationships among the stored concepts; identifying the disease related pathway affected by a drug or drug discovery target; querying the database to identify alternative pathways that are also affected by the drug or the drug discovery target and that result in the undesirable phenotype.

48. (Withdrawn) A method for identifying or validating a genotypic marker for a disease state that comprises providing a means for storing and accessing genomics information in a database wherein said means permits computational analysis of biological relationships among the stored concepts; querying the database to identify a genotypic marker that is associated with a disease state.

49. (Withdrawn) A method for identifying a drug discovery target which comprises querying a computer system to identify a disease-related pathway and identifying the biological interactions and actor concepts in the disease-related pathway whereby at least one of the actor concepts involved in each such reaction is a drug discovery target and wherein the computer system comprises a means for storing and accessing genomics information in a database and a means for computational analysis of biological relationships among the stored concepts.

50. (Withdrawn) A method of conducting business that comprises receiving compensation from a customer in return for identifying to the customer a drug discovery target discovered by querying a computer system to identify a disease-related pathway and identifying the biological interactions and actor concepts in the disease-related pathway whereby each of the actor concepts involved in each such reaction is a drug discovery target and wherein the computer system comprises a means for storing and accessing genomics information in a database and a means for computational analysis of biological relationships among the stored concepts.

51. (Withdrawn) A drug discovery target identified by the process of claim 1.

52. (Withdrawn) A method of drug discovery that comprises:

(a) identifying a drug discovery target discovered by querying a computer system to identify a disease-related pathway and identifying the biological interactions and actor concepts in the disease-related pathway whereby one or more of the actor concepts involved in each such reaction is a drug discovery target and wherein the computer system comprises a means for storing and accessing genomics information in a database and a means for computational analysis of biological relationships among the stored concepts; and

(b) screening compounds against a drug discovery target to identify drug candidates.

53. (Withdrawn) A candidate identified by the process of claim 52.

54. (Currently Amended) The computer system of claim 33, wherein the computer is further configured to analyze the user-supplied genomics data to identify a new use for a known therapy wherein the differential gene expression data relates to a pathway affected by the known therapy.

55. (Currently Amended) The computer system of claim 33, wherein the computer is further configured to analyze the user-supplied genomics data ~~to~~ prioritizinge candidate development compounds for further development by giving higher priority to development compounds on the basis of whether or not they are likely to result in an undesirable effect based on their involvement in other biological pathways as embodied in one of the one or more overlapped profiles.

56. (Currently Amended) The computer system of claim 33, wherein the computer is further configured to analyze the user-supplied genomics data to identify disease-related pathways wherein the disease is a side effect of drug therapy.

57. (Currently Amended) The computer system of claim 33, wherein the differential gene expression data relates to a particular disease, and wherein the ~~analyzing step~~ analysis of one or more statistically significant overlapped profiles together with the user-supplied genomics data further ~~includes~~ comprises ~~the step of~~ validating whether the differential gene expression data comprise~~are~~ genotypic markers for the disease ~~state~~ according to whether a database asserted biological association related to the disease ~~state~~, which is shared among a plurality of overlapped profiles, is statistically significant.

58. (New) A computer system for evaluating user-supplied genomics data, the system comprising:

a computer comprising a structured database to store and access genomics information, wherein the computer permits the computation of complex relationships among genes and/or gene products found within the genomics information

wherein the computer is configured to:

(a) define a profile model based on one or more profile definition criteria;

(b) build a collection of profiles according to the profile model using the genomics information stored in the structured database, wherein each profile comprises a subset of the genomics information contained in the structured database comprising information relating to genes, their DNA sequences, their mRNA, proteins expressed from said genes and the biological effects of the expressed proteins;

(c) receive the user-supplied genomics data;

(d) identify a plurality of overlapped profiles from the collection of profiles that comprise an overlap with at least a portion of the user-supplied genomics data and

(e) rank at least a subset of the plurality of overlapped profiles, based on statistical significance ofthe overlap according to one or more metrics; and

wherein the computer system is a stand alone computer, a multicomponent computer, or a networked computer, and wherein the computer system further comprises hardware for electronically searching the knowledge base.

59. (New) The computer system of claim 58, wherein the computer is further configured to analyze database asserted biological interactions embodied in at least a subset of the plurality of overlapped profiles with an overlap to the user-supplied genomics data that is above a threshold statistical significance.